RAW SEQUENCE LISTING

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Application Serial Number: _10/732,859B_
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RAW SEQUENCE LISTING   DATE: 12/06/2006
PATENT APPLICATION: **US/10/732,859B**   TIME: 08:45:54

Input Set : **A:\48202.app**
Output Set: **N:\CRF4\12062006\J732859B.raw**

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 3 <110> APPLICANT: TURCK, JUTTA
 4        ARCHER, JOHN
 6 <120> TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES
 8 <130> FILE REFERENCE: 13101/48202
10 <140> CURRENT APPLICATION NUMBER: 10/732,859B
11 <141> CURRENT FILING DATE: 2003-12-09
13 <150> PRIOR APPLICATION NUMBER: 09/469,211
14 <151> PRIOR FILING DATE: 1999-12-22
16 <150> PRIOR APPLICATION NUMBER: 9828660.2
17 <151> PRIOR FILING DATE: 1998-12-24
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 7599
25 <212> TYPE: DNA
26 <213> ORGANISM: Rhodococcus sp.
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (295)..(1035)
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1261)..(2805)
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (2807)..(4720)
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (5721)..(6665)
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47 cgcccgcaga gggcgcatgt ccgggtgcct ggatatggcg cgtacggcgt gccctccggc   120
49 gttaaccccg aggttggcca cgatgccccg gccatcaggt ctggaatgct agcgttccag   180
51 acgaaggtaa cccacagtga ctcacaccac aagtactaga atgcaagctg ttgcggtgag   240
53 cgccgcggca taggggggag ccatgtccgg gacgccgacg gaaagcctga ctcg atg     297
54                                                             Met
55                                                             1
57 acc acc acc gac acc ggc ccc aag ccg ggc agt gag gcc gcc gcc ctg    345
58 Thr Thr Thr Asp Thr Gly Pro Lys Pro Gly Ser Glu Ala Ala Ala Leu
59             5                  10                 15
61 ctc gcc aat gtc cgc acc tcg ggg gcg cgg ctg tcc tcc gcg ttg tac    393
62 Leu Ala Asn Val Arg Thr Ser Gly Ala Arg Leu Ser Ser Ala Leu Tyr
63         20                 25                 30
65 gac att ctg aag aac cgg ctg ctc gaa ggg cgc tat gcg gca ggc gag    441
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 66 Asp Ile Leu Lys Asn Arg Leu Leu Glu Gly Arg Tyr Ala Ala Gly Glu
 67     35                      40                  45
 69 aag atc gtc gtc gag tcg atc cgg caa gag ttc ggg gtg agc aag cag      489
 70 Lys Ile Val Val Glu Ser Ile Arg Gln Glu Phe Gly Val Ser Lys Gln
 71 50                      55                  60                  65
 73 ccc gtc atg gac gct ctg cgc cgc ctg tcc agc gac aag ctg gtc cac      537
 74 Pro Val Met Asp Ala Leu Arg Arg Leu Ser Ser Asp Lys Leu Val His
 75                     70                  75                  80
 77 atc gtt ccc cag gtc ggt tgc gag gtc gtc tcc tac gcc ccg cgc gaa      585
 78 Ile Val Pro Gln Val Gly Cys Glu Val Val Ser Tyr Ala Pro Arg Glu
 79                 85                  90                  95
 81 gtg gaa gac ttc tac acc ctg ttc ggc ggt ttc gaa ggg acc atc gcc      633
 82 Val Glu Asp Phe Tyr Thr Leu Phe Gly Gly Phe Glu Gly Thr Ile Ala
 83             100                 105                 110
 85 gcg gta gcg gcc tcc cgg cgg acc gag gcc cag ttg ctg gag ctg gac      681
 86 Ala Val Ala Ala Ser Arg Arg Thr Glu Ala Gln Leu Leu Glu Leu Asp
 87     115                 120                 125
 89 ctg atc tcg gcg cgg gtc gac gcc ctg atc acc tcc cac gac ccg gtg      729
 90 Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr Ser His Asp Pro Val
 91 130                 135                 140                 145
 93 gtc cgc gcc cgc ggg tac cgc gtg cac aac cgg gag ttc cat gcg gcc      777
 94 Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg Glu Phe His Ala Ala
 95                 150                 155                 160
 97 atc cac gcg atg gcg cac tcg cgg atc atg gag gag acc agc cag cga      825
 98 Ile His Ala Met Ala His Ser Arg Ile Met Glu Glu Thr Ser Gln Arg
 99             165                 170                 175
101 atg tgg gat ctg tcg gac ttc ttg atc aac acc acc ggc atc acc aac      873
102 Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile Thr Asn
103         180                 185                 190
105 ccg ctc tcg agc gca ctg ccc gac cgg cag cat gac cac cac gaa atc      921
106 Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His Glu Ile
107     195                 200                 205
109 acc gag gcc atc cgc aac cgt gac gca gct gcc gcc cgc gag gcc atg      969
110 Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Ala Arg Glu Ala Met
111 210                 215                 220                 225
113 gaa cgc cac atc gtc ggc acc atc gca gta atc cgc gac gaa tcc aac     1017
114 Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu Ser Asn
115                 230                 235                 240
117 gcc cag ctg ccg agc tag accccgatac ccgggccatc gaccggctcc            1065
118 Ala Gln Leu Pro Ser
119             245
121 gctatcgcgc cacctacgcc gaggggggac tctcggccgt agcgctgcag acgatccacc   1125
123 ggcaccctcc acgctgaccc ctgtctcgcc ctagagggcc ggcgcgccgt cgatcacctt   1185
125 taccctcatc cagagacttg cgtcaccctc tatgcccgag tagcgtctga actagacgtc   1245
127 tagcattcta gttga gtg ctc cct ctc gaa gat tct cca gag aac ccc tct    1296
128                  Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser
129                          250                 255
131 cga aca tcc cca gaa gaa agg agc ggc cat gac gac cgc ttc gca cgc     1344
132 Arg Thr Ser Pro Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg
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133      260                   265                   270
135 atc gtc ctt cgg ggc acg agc cca ctt ccg ccc aca gat cgg gga agc    1392
136 Ile Val Leu Arg Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser
137 275                   280                   285                   290
139 ccg acc gtg agc acc aca cct acc tcc ccg acg aag acc tca ccg ctg    1440
140 Pro Thr Val Ser Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu
141                   295                   300                   305
143 cgg gta gcg atg gcc agc ttc atc ggt acc acc gtc gag tac tac gac    1488
144 Arg Val Ala Met Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp
145                   310                   315                   320
147 ttc ttc atc tac ggc acc gcg gcc gcg ctg gta ttc cct gag ttg ttc    1536
148 Phe Phe Ile Tyr Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe
149             325                   330                   335
151 ttc ccg gat gtc tcg tcc gcg atc gga atc ctg ttg tcg ttc gcg acc    1584
152 Phe Pro Asp Val Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr
153       340                   345                   350
155 ttc agc gtt ggg ttc ctc gcc cgc ccg ctg ggt ggc ata gtg ttc ggg    1632
156 Phe Ser Val Gly Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly
157 355                   360                   365                   370
159 cac ttc ggt gac cgg gtc ggc cgc aag cag atg ctg gtg atc tcc ctg    1680
160 His Phe Gly Asp Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu
161                   375                   380                   385
163 gtc gga atg ggc tcg gcc acc gta ctg atg gga ttg ttg ccc ggt tac    1728
164 Val Gly Met Gly Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr
165             390                   395                   400
167 gcc caa atc ggg atc gcc gcc ccc atc ctg ctg acc ctg ctg cgc ctg    1776
168 Ala Gln Ile Gly Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu
169       405                   410                   415
171 gtg cag ggc ttt gcc gtc ggc ggc gag tgg ggt gga gcc acc ctg atg    1824
172 Val Gln Gly Phe Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met
173       420                   425                   430
175 gcc gtc gag cac gcc ccc acc gcg aag aag ggc ttt ttc gga tcc ttc    1872
176 Ala Val Glu His Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe
177 435                   440                   445                   450
179 tcc cag atg ggg gca ccc gcc ggg acc agc gtc gca acc ctg gcg ttc    1920
180 Ser Gln Met Gly Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe
181             455                   460                   465
183 ttc gcg gtc tcc caa ttg ccc gac gag cag ttc ctg agt tgg ggc tgg    1968
184 Phe Ala Val Ser Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp
185             470                   475                   480
187 cga ctg ccg ttc ctg ttc agc gcg gtg ctg atc gtg atc ggg ctg ttc    2016
188 Arg Leu Pro Phe Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe
189       485                   490                   495
191 att cgc ctg tcc ctg gcc gaa agc ccc gac ttc gcc gag gtg aag gca    2064
192 Ile Arg Leu Ser Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala
193       500                   505                   510
195 cag agc gcc gtg gtg cga atg ccg atc gcc gaa gcg ttc cgc aag cac    2112
196 Gln Ser Ala Val Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His
197 515                   520                   525                   530
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199 tgg aag gaa att ctc ctc atc gcg ggc acc tac ctg tcc caa gga gtg     2160
200 Trp Lys Glu Ile Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val
201             535                 540                 545
203 ttc gcc tat atc tgc atg gcc tac ctc gtc tcc tac ggc acc acc gtc     2208
204 Phe Ala Tyr Ile Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val
205             550                 555                 560
207 gcg ggg atc agc cgc acc ttc gcc ctg gcc gga gta ttc gtc gcc ggc     2256
208 Ala Gly Ile Ser Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly
209             565                 570                 575
211 atc gtc gcc gtc ctc ctc tac ctc gtg ttc ggc gct ctg tcc gac act     2304
212 Ile Val Ala Val Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr
213     580                 585                 590
215 ttc ggc cgc aag acc atg tac ctg ctc ggc gcc gcc gcg atg ggt gtg     2352
216 Phe Gly Arg Lys Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val
217 595                 600                 605                 610
219 gtg atc gcc ccc gcc ttc gca ctg atc aac acc ggc aac ccg tgg ctg     2400
220 Val Ile Ala Pro Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu
221             615                 620                 625
223 ttc atg gcc gcg cag gtg ctg gtc ttc gga att gca atg gcc ccc gcc     2448
224 Phe Met Ala Ala Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala
225             630                 635                 640
227 gcc ggc gtg aca ggc tcc ctg ttc acg atg gtc ttc gac gcg gac gtg     2496
228 Ala Gly Val Thr Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val
229             645                 650                 655
231 cgc tac agc ggt gtc tct atc ggc tac acc atc tcc cag gtc gcc ggc     2544
232 Arg Tyr Ser Gly Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly
233     660                 665                 670
235 tcc gcg ttc gcc ccg acg atc gcg acc gcc ttg tac gcc tcc acc aac     2592
236 Ser Ala Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn
237 675                 680                 685                 690
239 acc agc aac tcg atc gtg acc tac ctg ctg atc gtc tcg gcc atc tcg     2640
240 Thr Ser Asn Ser Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser
241             695                 700                 705
243 atc gtc tcg gtg atc ctg ctg ccc ggc ggc tgg ggg cgc aag ggc gct     2688
244 Ile Val Ser Val Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala
245             710                 715                 720
247 gcg agc cag ctc act cgc gac cag gcc acc tcc aca ccg aaa atg cct     2736
248 Ala Ser Gln Leu Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro
249             725                 730                 735
251 gac acc gaa aca ttt tcg act cgg aca gtt ccg gac acc gca gca tcc     2784
252 Asp Thr Glu Thr Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser
253     740                 745                 750
255 ctg cgc gtc ctc gac aag tga a gtg atg aca gac atg agt gac cac gac  2833
256 Leu Arg Val Leu Asp Lys         Val Met Thr Asp Met Ser Asp His Asp
257 755                 760                 765
259 cgc acc tcc tac gac acc gac gtc gtg atc gtc ggc ctc ggc ccc gcc     2881
260 Arg Thr Ser Tyr Asp Thr Asp Val Val Ile Val Gly Leu Gly Pro Ala
261 770                 775                 780                 785
263 ggt ggc aca gcg gcg ctt gcc ctg gcc agc tac ggc atc cgc gtt cac     2929
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264 Gly Gly Thr Ala Ala Leu Ala Leu Ala Ser Tyr Gly Ile Arg Val His
265               790                 795             ·        800
267 gcc gtc tcg atg ttc ccc tgg gtg gcg aac tcg ccg cgc gcg cac atc    2977
268 Ala Val Ser Met Phe Pro Trp Val Ala Asn Ser Pro Arg Ala His Ile
269               805                 810                 815
271 acc aac cag cgc gcc gtc gaa gtg ctg cgt gac ctg ggc gtc gaa gac    3025
272 Thr Asn Gln Arg Ala Val Glu Val Leu Arg Asp Leu Gly Val Glu Asp
273               820                 825                 830
275 gag gcg cgc aac tac gcc acc ccg tgg gac cag atg ggc gac acg ctg    3073
276 Glu Ala Arg Asn Tyr Ala Thr Pro Trp Asp Gln Met Gly Asp Thr Leu
277               835                 840                 845
279 ttc acc acg agc ctg gcc ggc gag gag atc gtc cgg atg cag acc tgg    3121
280 Phe Thr Thr Ser Leu Ala Gly Glu Glu Ile Val Arg Met Gln Thr Trp
281 850               855                 860                 865
283 ggt acg ggc gat atc cgc tac ggg gac tac ctg tcc gga agc ccc tgc    3169
284 Gly Thr Gly Asp Ile Arg Tyr Gly Asp Tyr Leu Ser Gly Ser Pro Cys
285               870                 875                 880
287 acg atg ctc gac att ccg cag ccc ctg atg gag ccg gtg ctg atc aag    3217
288 Thr Met Leu Asp Ile Pro Gln Pro Leu Met Glu Pro Val Leu Ile Lys
289               885                 890                 895
291 aac gcc gcc gaa cgt ggt gcg gtc atc agc ttc aac acc gaa tac ctc    3265
292 Asn Ala Ala Glu Arg Gly Ala Val Ile Ser Phe Asn Thr Glu Tyr Leu
293               900                 905                 910
295 gac cac gcc cag gac gag gac ggg gtg acc gtc cgg ttc cgc gac gtc    3313
296 Asp His Ala Gln Asp Glu Asp Gly Val Thr Val Arg Phe Arg Asp Val
297               915                 920                 925
299 cgc tcg ggc acc gtg ttc acc cag cga gcc cgc ttc ctg ctc ggt ttc    3361
300 Arg Ser Gly Thr Val Phe Thr Gln Arg Ala Arg Phe Leu Leu Gly Phe
301 930               935                 940                 945
303 gac ggc gca cga tcg aag atc gcc gaa cag atc ggg ctt ccg ttc gaa    3409
304 Asp Gly Ala Arg Ser Lys Ile Ala Glu Gln Ile Gly Leu Pro Phe Glu
305               950                 955                 960
307 ggt gaa ctc gcc cgc gcc ggt acc gcg tac atc ctg ttc aac gcg gac    3457
308 Gly Glu Leu Ala Arg Ala Gly Thr Ala Tyr Ile Leu Phe Asn Ala Asp
309               965                 970                 975
311 ctg agc aaa tat gtc gct cat cgg ccg agc atc ttg cac tgg atc gtc    3505
312 Leu Ser Lys Tyr Val Ala His Arg Pro Ser Ile Leu His Trp Ile Val
313               980                 985                 990
315 aac tcg aag gcc ggt ttc ggt  gag atc ggc atg ggt  ctg ctg cgc gcg   3553
316 Asn Ser Lys Ala Gly Phe Gly  Glu Ile Gly Met Gly  Leu Leu Arg Ala
317       995                 1000                 1005
319 atc  cga ccg tgg gac cag  tgg atc gcc ggc tgg  ggc ttc gac atg      3598
320 Ile  Arg Pro Trp Asp Gln  Trp Ile Ala Gly Trp  Gly Phe Asp Met
321 1010                 1015                 1020
323 gcg  aac ggc gag ccg gat  gtc tcc gac gac gtt  gtc ctc gaa cag      3643
324 Ala  Asn Gly Glu Pro Asp  Val Ser Asp Asp Val  Val Leu Glu Gln
325 1025                 1030                 1035
327 atc  cgg acc ctc gtc ggc  gac ccg cac ctg gac  gtc gag atc gtg      3688
328 Ile  Arg Thr Leu Val Gly  Asp Pro His Leu Asp  Val Glu Ile Val
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